IN THE CLAIMS:

The following listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claim 1-44 (cancels d)

Claim 45. (currently amended) The array according to claim 47-52 wherein the array contains a substrate for attaching nucleix: acid molecules thereto.

Claim 46. (currently amended) The array according to claim 46.45 wherein the substrate is glass.

Claim 47. (withdrawn) An array comprising at least 10 nucleic acid molecules wherein the at least 10 nucleic acid molecules are SEQ. ID Nos.: 115-124.

Claim 48. (withdrawn) An array according to claim 47 wherein the array further comprises SEQ ID Nos.:125-176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 213-384 and complements thereof

Claim 49. (withdrawn) An array comprising partial gene sequences from toxicologically relevant canine genes comprising (SEQ. ID Nos.: 115-124 and complements thereof.

Claim 50. (withdrewn) An array comprising a combination of partial gene sequences from toxicologically relevant canine genes comprising SEQ. ID Nos.: 116-118, 121 and 123 and complements thereof.

Claim 51. (withdrawn) An array according to claim 50 wherein the array further comprises SEQ. ID Nos.: 115, 119, 120, 122, 124-176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 213-384 and complements then

Claim 52. (currently amended) An array comprising a combination of canine nucleic acid molecules comprising SEQ. (SEQ ID Nos.:116-118, 121 and 123 and the complements thereof, and consisting of SEQ ID No. 329 and the complements thereof.

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Claim 53. (currently amended) An array as described in claim 52 wherein the array further comprises SEQ ID Nos.:115, 119, 1:20, 424-179 124-171, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 213-328, and the complements thereof.

Claim 54. (currently amended) A method for texicity detection of a compound nucleic acid in a canine sample, said method comprising:

- a) obtaining nucleic acids from a canine sample;
- b) contacting the nucleic acids of the <u>canlne</u> sample with an array the array of claim 52 or 53 comprising the combination of SEQ IDs of claim 53 under conditions to form one or more hybridization complexes; and
- c) detecting said hybridization complexes.; and
- d) comparing the Li vels of the hybridization complexes detected in step (c) with the level of hybridization complexes detected. I in a non-desed sample, wherein the altered level of hybridization complexes detected in step (c) compared with the level of hybridization complexes of a non-desed sample correlates with the presence of compared to the canino.